

An Application of Envelope Methodology and Aster Models

Daniel J. Eck

Department of Statistics, University of Minnesota

and

Charles J. Geyer

Department of Statistics, University of Minnesota

and

R. Dennis Cook

Department of Statistics, University of Minnesota

January 30, 2017

Abstract

Precise estimation of expected Darwinian fitness is a central component of life history analysis. Our methods provide precise estimation by incorporating general envelope methodology into the aster modeling framework. This level of precision provided from our methods allow researchers to draw stronger conclusions about the driving forces of Darwinian fitness from their life history analyses than they could with the aster model alone. The aster model serves as a defensible statistical model for distributions of Darwinian fitness. Envelope methodology reduces asymptotic variability by establishing a link between unknown parameters of interest and the asymptotic covariance matrices of their estimators. It is known both theoretically and in applications that incorporation of envelope methodology reduces asymptotic variability. A novel envelope estimator is developed and used to obtain variance reduction. Our methods are illustrated on a simulated dataset and a real dataset of *Mimulus guttatus* flowers. Variance reduction is obtained in both analyses. Our examples are fully reproducible in an accompanying technical report.

Keywords: Aster model; Darwinian fitness; Envelope model; Life history analysis

1 Introduction

The estimation of expected Darwinian fitness, the expected lifetime number of offspring an organism has, is a very important quantity in both biology and genetics. The importance of this quantity is not just limited to scientific disciplines, it is important for public policy. With genetic theory and simulation studies, Burger and Lynch (1995) shows that, under certain conditions, a changing environment leads to extinction of species. In a field study for some plants, Etterson and Shaw (2001) argued that the predicted evolutionary response to predicted rates of climate change are far too slow. In these papers, and all life history analyses of their kind, expected Darwinian fitness is the response variable. The interesting scientific conclusions are drawn from it.

In many life history analyses, values of expected Darwinian fitness are plotted using a fitness landscape. A fitness landscape is the conditional expectation of Darwinian fitness plotted across phenotypic trait values. As such, the fitness landscape is a regression function. The estimation of the fitness landscape began with Lande and Arnold (1983). Their modeling of expected Darwinian fitness was conducted via ordinary least squares (OLS) regression with the assumption that phenotypic traits are normally distributed. This assumption is unlikely to be met in practice (Mitchell-Olds and Shaw, 1987; Shaw, Geyer, Wagenius, Hangelbroek, and Etterson, 2008). The distribution of Darwinian fitness often has a large atom at 0 (corresponding to individuals that have died before reproducing), is multimodal (corresponding to breeding season), right-skewed, and integer-valued. These problems sternly call into question the appropriateness of OLS as a tool for inference on Darwinian fitness. The aster model was designed to fix all of these problems present with the Lande and Arnold (1983) approach. The aster model is the state-of-the-art model for all life history analyses in which the estimation of expected Darwinian fitness is the primary goal.

Researchers using an aster model in their analysis are estimating expected Darwinian fitness through maximum likelihood estimation. The aster model itself is a regular full exponential family. Properties of parameter estimation in this setting are well understood. Specifically, the maximum likelihood estimator (MLE) for the aster model mean-value pa-

parameter vector $\hat{\tau}$ is asymptotically normal with asymptotic covariance matrix given by Fisher information Σ . Estimates of both τ and Σ are provided in the **R** contributed **aster** package (Geyer, 2014). The analyses we consider estimate expected Darwinian fitness for categorical variables and fitness landscapes (Shaw, Geyer, Wagenius, Hangelbroek, and Etterson, 2008; Shaw and Geyer, 2010). Fitness landscapes are the conditional expectation of Darwinian fitness given a wide range of predictor values. This tool is used to see which combination of predictor values yield the highest estimated expected Darwinian fitness.

We further improve on the aster model through the incorporation of general envelope methodology. Envelope models were developed as a variance reduction tool for the multivariate linear regression model. These models are especially useful when some characteristics of the response vector are unaffected by changes in the predictors. The MLE from the envelope model can be substantially less variable than OLS estimator, especially when the mean function varies in directions that are orthogonal to the directions of maximum variation for the response vector (Cook, Li, and Chiaromonte, 2010). These efficiency gains can be massive. There are examples where the OLS estimator would require 10,000 times as many data points to replicate the standard errors obtained through envelope estimation. Su and Cook (2011) developed partial envelope models for analyses that have a distinction between parameters of interest and nuisance parameters. Cook and Zhang (2015) developed the most general envelope framework to date, which assumes only a \sqrt{n} consistent and asymptotically normal estimator of an unknown parameter vector and a \sqrt{n} consistent estimator of its asymptotic covariance matrix.

From both the data analysis standpoint and the theoretical standpoint, we show that the assumptions and quantities needed for general envelope methodology are inherent in aster modeling and are easily obtained. Our envelope methodology, which seeks variance reduction of expected Darwinian fitness, is implemented with respect to mean value parameters instead of canonical parameters. We also construct envelope estimators by searching over reducing subspaces of the estimated covariance matrix. Variance reduction is assessed using parametric bootstrap algorithms developed in this exposition. These bootstrap algorithms are

robust against model selection volatility by incorporating techniques in (Efron, 2014, Section 4). Our methodology provides the most precise estimation of expected Darwinian fitness to date when using aster models. Researchers using our methods can therefore draw stronger conclusions about the driving forces of Darwinian fitness from their life history analyses. In a real data example and a simulated example, we show that our methodology leads to variance reduction in estimation of expected Darwinian fitness when compared with analyses that use aster models alone. These examples use our new envelope estimator constructed from reducing subspaces. Our examples are fully reproducible and the calculations necessary for its reproduction are included in an accompanying technical report (see Supplementary Material Section).

2 The aster model

The aster model is a graphical model obeying the following five assumptions:

- A1. The graph is acyclic.
- A2. A node has at most one predecessor node.
- A3. The joint distribution is the product of conditional distributions, one conditional distribution for each arrow in the aster graph.
- A4. Predecessor is sample size.
- A5. Conditional distributions for arrows are one-parameter exponential family (possibly a different family for each arrow).

Assumptions A4 and A5 mean for an arrow $y_k \longrightarrow y_j$ that y_j is the sum of independent and identically distributed random variables from the exponential family for the arrow and there are y_k terms in the sum (the sum of zero terms is zero). These assumptions imply that the joint distribution of the aster model is an exponential family (Geyer, Wagenius, and Shaw, 2007, Section 2.3).

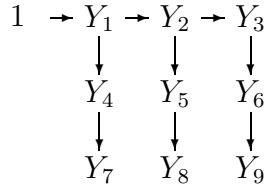


Figure 1: Graphical structure of the aster model for one individual in the *E. angustifolia* data. The top layer corresponds to survival; these random variables are Bernoulli. The middle layer corresponds to flowering; these random variables are also Bernoulli. The bottom layer corresponds to flower head counts; these random variables are zero-truncated Poisson.

As an example of an analysis using aster models, consider a population of *Echinacea angustifolia*, plants where total flower head count is taken to be Darwinian fitness as in Geyer, et al. (2007). The graph for one individual is shown in Figure 1. There are nine response variables per individual. The first three indicate survival in each of three years. The next three indicate flowering (zero is no flowers, one is some flowers). The last three are flower head counts. The conditional distributions are Bernoulli for the indicator variables (first six) and zero-truncated Poisson for the rest (last three). These are all exponential families (property A5). Property A4 and sum of zero terms is zero imply that predecessor equals zero implies successor equals zero. Hence the aster model has dead individuals remaining dead, has dead individuals having no flowers, and has individuals with no flowers having zero flower head count. Thus the aster model contains the major dependencies in life histories. The combination of a Bernoulli arrow followed by a zero-truncated Poisson arrow gives a zero-inflated Poisson distribution (e. g., the conditional distribution of Y_7 given Y_1). This factorization of zero-inflated Poisson into product of zero-truncated Poisson and Bernoulli is required by A5 (one parameter per arrow).

The aster models to which we apply general envelope methodology are unconditional aster models and unconditional aster submodels (Geyer, Wagenius, and Shaw, 2007; Geyer, 2010). Parameters associated with unconditional aster models are displayed in the middle and right columns of Figure 2. The parameters in the left column of Figure 2 correspond to conditional aster models. Almost all uses of aster models are unconditional aster models and our methods are developed for these models exclusively. The response vector of an

unconditional aster model has the same dimension as the canonical parameter vector φ that we are interested in estimating when using this model. These models are saturated (one parameter per component of the response vector) and hence not useful. Therefore, the unconditional aster submodel is used where we write $\varphi = a + M\beta$, see Figure 2. We will refer to the unconditional aster submodel as an aster model. Here $\varphi \in \mathbb{R}^m$ is the unconditional aster model canonical parameter and β is the aster model canonical parameter vector where m is the dimension of the response vector. The number of responses is the number of nodes that appear in the graphical structure multiplied by the number of individuals sampled. $M \in \mathbb{R}^{m \times p}$ is a known model matrix assumed to be of full column rank where p is the dimension of the aster model, and $a \in \mathbb{R}^m$ is a known offset vector.

There are five parameters of interest that are present in the aster analyses we consider, four parameterizations and one function of one of these. These parameterizations are:

- 1) The aster model canonical parameter vector $\beta \in \mathbb{R}^p$.
- 2) The aster model mean-value parameter vector $\tau \in \mathbb{R}^p$.
- 3) The saturated aster model canonical parameter vector $\varphi \in \mathbb{R}^m$.
- 4) The saturated aster model mean-value parameter vector $\mu \in \mathbb{R}^m$.
- 5) The best surrogate of expected Darwinian fitness, which is a function of μ .

Relations among the parameterizations are shown in Figure 2. In the *E. angustifolia* example, Darwinian fitness has one component per individual, which gives the total (over the three years) flower head count for that individual, so in this case it is a linear function.

The log likelihood for the aster model in canonical form is

$$l(\beta) = \langle M^T Y, \beta \rangle - c(a + M\beta)$$

with canonical statistic $M^T Y$ and $Y \in \mathbb{R}^m$ is the vector of responses depicted in the corresponding graphical structure. The response vector has one component for every node in the graph for every individual in the study. Our model, being a regular full exponential

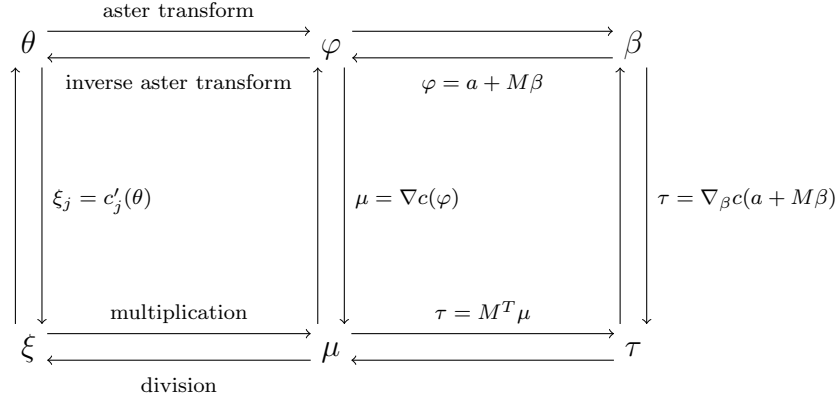


Figure 2: A depiction of the transformations necessary to change aster model parameterizations. These transformations are all invertible. Arrows going in opposite directions specify transformations and their inverses. M is a known model matrix of full column rank, a is a known offset vector, and c is the cumulant function for the unconditional aster model.

family, allows us to conveniently obtain the maximum likelihood estimator for our canonical parameter vector β . We obtain the model mean-value parameter τ by differentiation. We see that

$$\tau = \nabla_{\beta} c(a + M\beta) = M^T \nabla c(\varphi) = E(M^T Y) = M^T \mu$$

and the MLE of τ , denoted $\hat{\tau}$, is $M^T Y$. The MLE of β is obtained from invariance of maximum likelihood estimation where $\hat{\beta} = f^{-1}(\hat{\tau})$ and $f : \beta \mapsto M^T \nabla c(a + M\beta)$, seen in Figure 2, is an invertible mapping (assuming the model is identifiable). From the usual asymptotics of MLE and exponential families we have,

$$\sqrt{n}(\hat{\tau} - \tau) \xrightarrow{\mathcal{D}} N(0, \Sigma), \quad (1)$$

where $\Sigma = \text{Var}(M^T Y)$ is the Fisher information matrix associated with the canonical parameter vector β , which is the inverse Fisher information matrix for τ . The maximum likelihood estimator of β is asymptotically normal with variance given by Σ^{-1} . The **aster** software in **R** provides $\hat{\beta}$ and $\hat{\Sigma}$ where $\hat{\Sigma}$ is the maximum likelihood estimator of Σ . From (1) and the delta method we can obtain the asymptotic distribution for any differentiable function of $\hat{\tau}$.

The asymptotic distribution for a differentiable function g of $\hat{\tau}$ is

$$\sqrt{n}(g(\hat{\tau}) - g(\tau)) \xrightarrow{\mathcal{D}} N(0, \nabla g(\tau) \Sigma \nabla g(\tau)^T). \quad (2)$$

In particular, the asymptotic distribution of estimated expected Darwinian fitness is of interest, call it $h(\mu)$. Since $\beta = f^{-1}(\tau)$ and $\mu = \nabla c(a + M\beta)$,

$$g(\tau) = h\left(\nabla c(a + Mf^{-1}(\tau))\right)$$

gives expected Darwinian fitness as a function of τ and is differentiable if h is differentiable. So now our estimator $g(\hat{\tau})$ has asymptotic distribution given by (2).

3 Incorporation of general envelope methodology

The theory of general envelope methodology requires a \sqrt{n} consistent and asymptotically normal estimator of an unknown parameter vector and a \sqrt{n} consistent estimator of its asymptotic covariance matrix (Cook and Zhang, 2015). Aster models, being an exponential family, satisfy these conditions. Our methods distinguish parameters of interest from nuisance parameters. The parameters of interest are those components of τ which correspond directly to the estimation of Darwinian fitness. We partition τ into $(\gamma^T, v^T)^T$ where $\gamma \in \mathbb{R}^{p-k}$ and $v \in \mathbb{R}^k$ are the vectors of nuisance parameters and parameters of interest respectively. Envelope models that involve this form of partitioning are referred to partial envelope models (Su and Cook, 2011). The maximum likelihood estimator of the parameters of interest, \hat{v} , has asymptotic covariance matrix $\Sigma_{v,v}$ which is the submatrix of Σ corresponding to the parameters of interest. The estimator of $\Sigma_{v,v}$ obtained from **aster** software is denoted by $\hat{\Sigma}_{v,v}$.

Let $T = \text{span}(v)$. The envelope subspace $\mathcal{E}_{\Sigma_{v,v}}(T)$ is defined as the intersection of all reducing subspaces of $\Sigma_{v,v}$ that contain T (a reducing subspace is a sum of eigenspaces). We will denote the envelope subspace as \mathcal{E} when using it as a subscript. The envelope space satisfies both

1. $T \subset \mathcal{E}_{\Sigma_{v,v}}(T)$

$$2. \Sigma_{v,v} = P_{\mathcal{E}}\Sigma_{v,v}P_{\mathcal{E}} + Q_{\mathcal{E}}\Sigma_{v,v}Q_{\mathcal{E}}$$

where $P_{\mathcal{E}}$ is the projection into the envelope subspace and $Q_{\mathcal{E}}$ is the projection into the orthogonal complement. In coordinate form, the two envelope conditions are equivalent to

$$\text{a) } T \subset \text{span}(\Gamma)$$

$$\text{b) } \Sigma_{v,v} = \Gamma\Omega\Gamma^T + \Gamma_o\Omega_o\Gamma_o^T,$$

where (Γ, Γ_o) is a partitioned orthogonal matrix, the columns of Γ are a basis for $\mathcal{E}_{\Sigma_{v,v}}(T)$, and the dimensions of Ω and Ω_o are such that the matrix multiplications are defined.

The goal in envelope methodology is to estimate the basis matrix Γ of the envelope space $\mathcal{E}_{\Sigma_{v,v}}(T)$. The envelope space $\mathcal{E}_{\Sigma_{v,v}}(T)$ contains the parameter of interest and is a reducing subspace of $\Sigma_{v,v}$. Intuitively, the envelope estimator reduces variability in estimation at no cost to consistency by making use of the defining properties of $\mathcal{E}_{\Sigma_{v,v}}(T)$. With the basis matrix Γ estimated, we can construct envelope estimators of v and then map the resulting envelope estimators to the scale of Darwinian fitness. The variance reduction of estimated expected Darwinian fitness with respect to envelope estimation of v is then assessed.

To gain intuition on the working mechanics of envelope methodology, consider the case when Γ is known beforehand. When Γ is known, the envelope estimator of v is $P_{\mathcal{E}}\hat{v}$ with $P_{\mathcal{E}} = \Gamma\Gamma^T$, and

$$\sqrt{n}(P_{\mathcal{E}}\hat{v} - v) \xrightarrow{\mathcal{D}} N(0, P_{\mathcal{E}}\Sigma_{v,v}P_{\mathcal{E}}).$$

Knowledge of $u = \dim(\mathcal{E}_{\Sigma_{v,v}}(T))$ and $P_{\mathcal{E}}$ are both lacking in practice. Thus u and $P_{\mathcal{E}}$ are in need of estimation. The sequential 1D algorithm proposed in (Cook and Zhang, 2015, Algorithm 2) estimates the basis matrix Γ for $\mathcal{E}_{\Sigma_{v,v}}(T)$ at a user-supplied envelope dimension u . The estimate of Γ is obtained by providing $\hat{\Sigma}_{v,v}$ and $\hat{v}\hat{v}^T$ as inputs into the 1D algorithm. The resulting estimator of Γ obtained from the 1D algorithm, $\hat{\Gamma}$, is \sqrt{n} consistent and gives a \sqrt{n} consistent estimator $P_{\hat{\mathcal{E}}}$ of the projection onto the envelope subspace $P_{\mathcal{E}}$ (Cook and Zhang, 2015). The 1D algorithm finds the estimated basis $\hat{\Gamma}$ by performing u optimizations. Each of these optimizations separately finds an estimated basis vector for the envelope subspace that is orthonormal to the basis vectors that preceded it.

We can compare envelope dimensions u by transforming envelope estimators $\hat{v}_{\text{env}} = P_{\hat{\varepsilon}}\hat{v}$ to the canonical parameterization where $P_{\hat{\varepsilon}}$ is obtained from the 1D algorithm at candidate values of u . The envelope estimator of τ is given as

$$\hat{\tau}_{\text{env}} = \begin{pmatrix} \hat{\Gamma} \\ \hat{v}_{\text{env}} \end{pmatrix} = \begin{pmatrix} I & 0 \\ 0 & P_{\hat{\varepsilon}} \end{pmatrix} M^T Y = M_{\text{env}}^T Y$$

where

$$M_{\text{env}} = M \begin{pmatrix} I & 0 \\ 0 & P_{\hat{\varepsilon}} \end{pmatrix}$$

is the model matrix corresponding to the aster model that incorporates the partial envelope structure. The envelope estimator of τ is therefore a maximum likelihood estimate of the mean-value parameter corresponding to the aster model with model matrix M_{env} . The fact that the envelope estimator of τ is also a maximum likelihood estimator is of importance. It justifies the use of the transformations seen in Figure 2 used to switch between MLEs of aster model parameterizations. However, the model matrix M_{env} is not of full column rank. This means that the transformations in Figure 2 are not 1-1. In particular, many distinct estimates of β map to $\hat{\tau}_{\text{env}}$. Each of these distinct estimated values of β maps to the same estimate of $\varphi = M_{\text{env}}\beta$, which in turn maps to a common estimate of expected Darwinian fitness.

The mapping $f : \tau \rightarrow \beta$ cannot be expressed in closed form and we must use the **aster2** package (Geyer, 2010) to carry out the transformation finding $\hat{\beta}_{\text{env}} = f(\hat{\tau}_{\text{env}})$. From here, likelihood based methods for comparing models such as AIC, BIC, or the likelihood ratio test (LRT) are used to select which envelope model dimension is appropriate. The LRT has the hypotheses:

$$H_o : u = u_o$$

$$H_a : u = k$$

where $u_o \leq k$ is some proposed dimension of $\mathcal{E}_{\Sigma_{v,v}}(\mathbf{T})$. (The alternative is use the aster model.) At the envelope dimension u or a larger dimension, we have

$$\sqrt{n}(\hat{v}_{\text{env}} - v) \xrightarrow{\mathcal{D}} N(0, \Delta_1),$$

where Δ_1 is unknown. The asymptotic covariance matrix Δ_1 can be thought of as $\Delta_1 = P_{\mathcal{E}}\Sigma_{v,v}P_{\mathcal{E}} + C$ where $C > 0$ is the cost incurred from estimation.

However, inference with respect to v is not normally sought in life history analysis. What is sought is the estimated expected Darwinian fitness considered as a function of phenotypic trait values for a hypothetical individual. This function is referred to as the fitness landscape when traits are continuous. In the setting of continuous traits, the fitness landscape is plotted. This plot is the primary graphical inferential tool for our analyses. The envelope estimator of expected Darwinian fitness for these hypothetical individuals has asymptotic distributions given by

$$\sqrt{n}(g(\hat{\tau}_{\text{env}}) - g(\tau)) \xrightarrow{\mathcal{D}} N(0, \nabla g(\tau)\Delta_2\nabla g(\tau)^T), \quad (3)$$

where Δ_2 is the unknown asymptotic covariance matrix of $\hat{\tau}_{\text{env}}$. The asymptotic covariance matrix of estimated expected Darwinian fitness is estimated using a parametric bootstrap adjusting for model selection. The dimension of the envelope space is selected using model selection criteria and is not known in advance. (Efron, 2014, Section 4) provides a double bootstrap procedure which accounts for the randomness associated with model selection procedures. This double bootstrap procedure is used to estimate the variance of estimated expected Darwinian fitness using envelope methodology. At first, datasets are generated as a realization from the aster model distribution evaluated at the envelope estimator. The envelope dimension is determined for each of these generated datasets. The estimator of expected Darwinian fitness is then taken to be the average of all of the envelope estimators obtained from these datasets. To estimate the variability of this envelope estimator, we generate further datasets from the aster model distribution evaluated at each separate envelope estimator of expected Darwinian fitness used to calculate the aforementioned average. The steps of this procedure are presented in Algorithm 1 in Figure 3. More particulars on the application of the double bootstrap procedure outlined in Efron (2014) are included in the Discussion.

This algorithm requires that our aster model is fitted using a large enough sample size to provide a reliable maximum likelihood estimate of τ . This assumption is implicitly made

1. Fit the aster model to the data and obtain \hat{v} and $\hat{\Sigma}_{v,v}$ from the aster model fit.
2. Compute the envelope estimator of v in the original sample, given as $\hat{v}_{\text{env}} = P_{\hat{\varepsilon}}\hat{v}$ where $P_{\hat{\varepsilon}}$ is computed by the 1D algorithm. The 1D algorithm takes $M = \hat{\Sigma}_{v,v}$, $U = \hat{v}\hat{v}^T$, and dimension u as inputs. The dimension is selected using a model selection criterion of choice.
3. Perform a parametric bootstrap by generating resamples from the distribution of the aster model evaluated at $\hat{\tau}_{\text{env}} = (\hat{\gamma}^T, \hat{v}_{\text{env}}^T)^T$. For iteration $b = 1, \dots, B$ of the procedure:
 - (3a) Compute $\hat{\tau}^{(b)}$ and $\hat{\Sigma}_{v,v}^{(b)}$ from the aster model fit to the resampled data.
 - (3b) Obtain $P_{\hat{\varepsilon}}^{(b)}$ from the 1D algorithm as done in Step 2 using $M = \hat{\Sigma}_{v,v}^{(b)}$ and $U = \hat{v}^{(b)}\hat{v}^{(b)T}$ as inputs where the dimension of the envelope is selected using the same model selection criterion as Step 2.
 - (3c) Compute $\hat{v}_{\text{env}}^{(b)} = P_{\hat{\varepsilon}}^{(b)}\hat{v}^{(b)}$ and $\hat{\tau}_{\text{env}}^{(b)} = \left(\hat{\gamma}^{(b)T}, \hat{v}_{\text{env}}^{(b)T}\right)^T$
 - (3d) Store $\hat{\tau}_{\text{env}}^{(b)}$ and $g\left(\hat{\tau}_{\text{env}}^{(b)}\right)$ where g maps τ to the parameterization of Darwinian fitness.
4. After B steps, the bootstrap estimator of expected Darwinian fitness is the average of the envelope estimators stored in Step 3d. This completes the first part of the bootstrap procedure.
5. We now proceed with the second level of bootstrapping at the b -th stored envelope estimator $\hat{\tau}_{\text{env}}^{(b)}$. For iteration $k = 1, \dots, K$ of the procedure:
 - (5a) Generate data from the distribution of the aster model evaluated at $\hat{\tau}_{\text{env}}^{(b)}$.
 - (5b) Perform Steps 3a through 3c with respect to the dataset obtained in Step 5a.
 - (5c) Store $\hat{\tau}_{\text{env}}^{(b)(k)}$ and $g\left(\hat{\tau}_{\text{env}}^{(b)(k)}\right)$.

Figure 3: Algorithm 1. Parametric bootstrap envelope estimation of v using the 1D algorithm.

when performing an aster analysis whether or not one incorporates an envelope model structure. When our bootstrap procedure has run for a total of B iterations we obtain the envelope estimator

$$\frac{1}{B} \sum_{b=1}^B g(\hat{\tau}_{\text{env}}^{(b)}) \quad (4)$$

as suggested by (Efron, 2014, Section 4). The individual summands in (4) are estimates of expected Darwinian fitness obtained after model selection. The averaging in (4) smooths out erratic jumpiness that may occur from model selection (Efron, 2014). The envelope estimator (4), obtained from the parametric bootstrap in Algorithm 1, has variability analogous to that in (Efron, 2014, equation (4.15)). As in Efron (2014), we define the matrix $\mathbf{B}^{(b)} \in \mathbb{R}^{K \times p}$ which has rows $\hat{\tau}_{\text{env}}^{(b)(k)} - \sum_{k=1}^K \hat{\tau}_{\text{env}}^{(b)(k)} / K$ and the matrix $C^{(b)} \in \mathbb{R}^{K \times d}$ which has columns $g\left(\hat{\tau}_{\text{env}}^{(b)(k)}\right) - g\left(\hat{\tau}_{\text{env}}^{(b)}\right)$. We now estimate Δ_2 with

$$\hat{\Delta}_2 = \frac{1}{B} \sum_{b=1}^B \left[\widehat{\text{cov}}^{(b)} \right]^T \hat{V}^{(b)-1} \widehat{\text{cov}}^{(b)} \quad (5)$$

where

$$\widehat{\text{cov}}^{(b)} = \left[\mathbf{B}^{(b)} \right]^T C^{(b)} / K \quad (6)$$

and

$$\hat{V}^{(b)} = \left[\mathbf{B}^{(b)} \right]^T \mathbf{B}^{(b)} / K. \quad (7)$$

The estimator (5) of Δ_2 takes into account the volatility of model selection when estimating the variability of estimated expected Darwinian fitness using envelope methodology. The method of maximum likelihood estimation does not have the added model selection step that envelope estimation has. The bootstrap procedure outlined in Figure 3 efficiently estimates expected Darwinian fitness and accounts for variability associated with model selection volatility.

4 A novel alternative to general envelope estimation using reducing subspaces

We propose a new way of constructing envelope estimators provided that the eigenvalues of $\Sigma_{v,v}$ are unique. Envelope estimators are constructed directly from the reducing subspaces of $\hat{\Sigma}_{v,v}$. This new envelope estimator of v is $\hat{v}_{\text{env}} = P_{\hat{G}}\hat{v}$ where G is the smallest reducing subspace of $\Sigma_{v,v}$ such that $P_G v = v$. The reducing subspaces of $\hat{\Sigma}_{v,v}$ are \sqrt{n} consistent estimators of the reducing subspaces of $\Sigma_{v,v}$. Therefore $P_{\hat{G}}$, and the corresponding estimator $P_{\hat{G}}\hat{v}$ are \sqrt{n} estimators of P_G and $P_G v$ respectively. Our envelope estimator of τ becomes $\hat{\tau}_{\text{env}} = (\hat{\gamma}^T, \hat{v}_{\text{env}}^T)^T$ where $\hat{\gamma}$ is the MLE of the nuisance parameters obtained from the original aster model fit.

There is a close connection between envelope estimation using reducing subspaces and envelope estimation using the 1D algorithm. In the population, the envelope estimator of v using reducing subspaces is the same as the envelope estimator obtained from the 1D algorithm. The connection between both estimation methods exists in applications as well. Suppose that the envelope space is the reducing subspace G with dimension u and let $\hat{\Gamma}_u$ and $\Gamma_{\hat{G}}$ be the estimated basis matrices for the envelope space using the 1D algorithm and reducing subspaces respectively. Let $\hat{O} = \hat{\Gamma}_u \Gamma_{\hat{G}}^T$ be the matrix that changes from the coordinates of $\Gamma_{\hat{G}}$ to the coordinates of $\hat{\Gamma}_u$. The matrix \hat{O} is a \sqrt{n} -consistent estimator of the identity matrix of dimension k . Let $\hat{M} = \hat{O}^T \hat{\Sigma}_{v,v} \hat{O}$ and $\hat{U} = \hat{O}^T \hat{v} \hat{v}^T \hat{O}$. Then the 1D algorithm returns $\Gamma_{\hat{G}}$ as an estimated basis matrix for the envelope space when using \hat{M} and \hat{U} as inputs. Asymptotic normality of $\hat{P}_{\hat{G}}$ follows from (Cook and Zhang, 2015, Propositions 5 and 6) since \hat{M} and \hat{U} are both \sqrt{n} -consistent estimators of $\Sigma_{v,v}$ and U respectively.

In applications, envelope estimators obtained from reducing subspaces of $\hat{\Sigma}_{v,v}$ are compared using AIC, BIC, or the LRT. Our procedure for envelope estimation of expected Darwinian fitness using reducing subspaces of $\hat{\Sigma}_{v,v}$ is as follows:

1. Start with $u = 1$ and compute $\hat{v}_{\text{env}} = P_{\hat{G}}\hat{v}$ for all u dimensional reducing subspaces \hat{G} .

2. Compare all envelope estimators constructed in step 1 to \hat{v} using a selection criterion like AIC, BIC, or the LRT. If the envelope estimator is preferred, then stop and proceed with the analysis using the envelope estimator. If \hat{v} is preferred, then return to Step 1 and iterate u when $u < k$. If \hat{v} is preferred and $u = k$ then stop and proceed with the analysis using the MLE.
3. Perform the parametric bootstrap procedure outlined in Algorithm 2.

If the dimension of the problem is small enough, one can simply bypass the above procedure and compute all reducing subspaces at once. We bypass this procedure in both of our examples since the dimension of the problem is small enough to do so. The envelope estimators with respect to all of the reducing subspaces can then be compared using AIC, BIC, and LRT in one step. In either scenario, the reducing subspace approach considers $2^k - k$ more candidate envelope estimators than the 1D algorithm does. For this reason the researcher must use the 1D algorithm when k is large.

Once a decision is made on which reducing subspace \hat{G} to use, we need to estimate the variability of the envelope estimator $\hat{v}_{\text{env}} = P_{\hat{G}}\hat{v}$ using a parametric bootstrap. The steps for the parametric bootstrap employed are presented in Algorithm 2. Note that the reducing subspace \hat{G} is not used to build envelope estimators at each iteration of the parametric bootstrap procedure. The indices of the eigenvectors of $\hat{\Sigma}_{v,v}$ that comprise the reducing subspace \hat{G} are used instead. At each iteration of the parametric bootstrap the estimate of $\Sigma_{v,v}$ changes which implies that the estimate of the reducing subspace G changes. The parametric bootstrap procedure outlined in Algorithm 2, seen in Figure 4, takes into account model selection volatility by implementing a double bootstrap procedure analogous to that in Efron (2014).

When our bootstrap procedure has run for a total of B iterations, we obtain the envelope estimator of expected Darwinian fitness given by (4) with covariance matrix Δ_2 estimated by (5).

Envelope estimators constructed using reducing subspaces are different than those constructed using the 1D algorithm. At any iteration of the 1D algorithm, minimizers of the

1. Fit the aster model to the data and obtain \hat{v} and $\hat{\Sigma}_{v,v}$ from the aster model fit.
2. Compute the envelope estimator of v in the original sample, given as $\hat{v}_{\text{env}} = P_{\hat{G}}\hat{v}$ where $P_{\hat{G}}$ is computed using reducing subspaces and selected via a model selection criterion of choice.
3. Perform a parametric bootstrap by generating resamples from the distribution of the aster model evaluated at $\hat{\tau}_{\text{env}} = (\hat{\gamma}^T, \hat{v}_{\text{env}}^T)^T$. For iteration $b = 1, \dots, B$ of the procedure:
 - (3a) Compute $\hat{\tau}^{(b)}$ and $\hat{\Sigma}_{v,v}^{(b)}$ from the aster model fit to the resampled data.
 - (3b) Build $P_{\hat{G}}^{(b)}$ using the indices of $\hat{\Sigma}_{v,v}^{(b)}$ that are selected using the same model selection criterion as Step 2 to build \hat{G} .
 - (3c) Compute $\hat{v}_{\text{env}}^{(b)} = P_{\hat{G}}^{(b)}\hat{v}^{(b)}$ and $\hat{\tau}_{\text{env}}^{(b)} = \left(\hat{\gamma}^{(b)T}, \hat{v}_{\text{env}}^{(b)T}\right)^T$.
 - (3d) Store $\hat{\tau}_{\text{env}}^{(b)}$ and $g\left(\hat{\tau}_{\text{env}}^{(b)}\right)$ where g maps τ to the parameterization of Darwinian fitness.
4. After B steps, the bootstrap estimator of expected Darwinian fitness is the average of the envelope estimators stored in Step 3d. This completes the first part of the bootstrap procedure.
5. We now proceed with the second level of bootstrapping at the b -th stored envelope estimator $\hat{\tau}_{\text{env}}^{(b)}$. For iteration $k = 1, \dots, K$ of the procedure:
 - (5a) Generate data from the distribution of the aster model evaluated at $\hat{\tau}_{\text{env}}^{(b)}$.
 - (5b) Perform Steps 3a through 3d with respect to the dataset obtained in Step 5a.
 - (5c) Store $\hat{\tau}_{\text{env}}^{(b)(k)}$ and $g\left(\hat{\tau}_{\text{env}}^{(b)(k)}\right)$.

Figure 4: Algorithm 2. Parametric bootstrap envelope estimation of v using reducing subspaces.

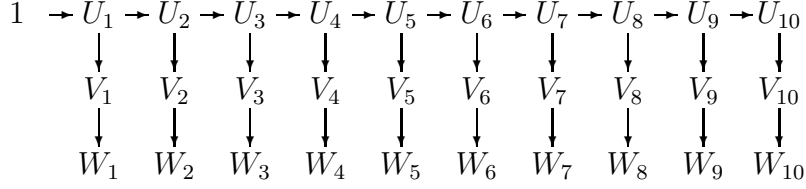


Figure 5: Graphical structure of the aster model for the simulated data in Example 1. The top layer corresponds to survival; these random variables are Bernoulli. The middle layer corresponds to whether or not an individual reproduced; these random variables are also Bernoulli. The bottom layer corresponds to offspring count; these random variables are zero-truncated Poisson.

objective function stated in (Cook and Zhang, 2015, Algorithm 2) are pulled towards reducing subspaces of $\hat{\Sigma}_{v,v}$. This objective function is non-convex and contains potentially many local minima. The optimizations conducted within the 1D algorithm are sensitive to starting values and can get stuck at these local minima. This undermines the 1D algorithm since it is required that users find global minima for its justification. Unlike the 1D algorithm, the reducing subspace approach does not involve any optimization routines necessary to the construction of envelope estimators and is preferred in settings when k is small.

5 Examples

We now provide two examples of our methods. In Example 1, there is a true envelope model incorporated in the simulation of the dataset. In Example 2, we show that our methods yield efficiency gains in a real data example.

5.1 Example 1

A population of 3000 organisms was simulated to form the dataset used in this aster analysis. We generated data according to a known reducing subspace and show that our methods recover the true indices of the reducing subspace that generated the data. These data

are generated according to the graphical structure appearing in Figure 5. There are two covariates (z_1, z_2) associated with Darwinian fitness and the aster model selected by the LRT is a full quadratic model with respect to these covariates. A full aster analysis of data of the same kind and its construction can be seen in Geyer and Shaw (2009).

In our example we consider the partial envelope approach. We partition τ into $(\gamma^T, v^T)^T$ where $\gamma \in \mathbb{R}^4$ are nuisance parameters and $v \in \mathbb{R}^5$ are relevant to the estimation of expected Darwinian fitness. Here, $v \in \mathbb{R}^5$ because our model is full quadratic in z_1 and z_2 . The true reducing subspace is the space spanned by the first and fourth eigenvectors of the covariance matrix of the parameters of interest estimated from the original data. We begin by considering envelope estimators constructed using the 1D algorithm. AIC, BIC, and the LRT at $\alpha = 0.05$ all select $u = 5$. This selection is equivalent to supposing that no non-trivial envelope structure is present and one should proceed with the aster analysis using maximum likelihood estimation and conventional **aster** software. The parametric bootstrap procedure discussed in Figure 3 is not interesting in this case. We now consider envelope estimators constructed from reducing subspaces.

AIC, BIC, and the LRT at $\alpha = 0.05$ all select a reducing subspace that is the sum of more eigenspaces than the true reducing subspace but fewer eigenspaces than the full space. There is also some disagreement between the model selection criteria. BIC and the LRT at $\alpha = 0.05$ select the reducing subspace that is the sum of the first, fourth, and fifth eigenspaces of $\hat{\Sigma}_{v,v}$, denoted \hat{G}_1 . AIC selects the reducing subspace that is the sum of every eigenspace of $\hat{\Sigma}_{v,v}$ except for the third eigenspace, denoted \hat{G}_2 . The parametric bootstrap algorithm discussed in Figure 4 is used to estimate the asymptotic variability of $g(\hat{\tau}_{\text{env}})$ using the reducing subspace \hat{G}_1 . The results are seen in Table 1 for selected output. Table 1 shows points that yield high values of estimated expected Darwinian fitness. The first two columns display the sample envelope estimator of expected Darwinian fitness and its bootstrapped standard error. The MLE of expected Darwinian fitness and its bootstrapped standard error are displayed in the third and fourth columns respectively. The ratios of bootstrapped standard errors for $g(\hat{\tau}_{\text{MLE}})$ to $g(\hat{\tau}_{\text{env}})$ are displayed in the final column. We can see that

Table 1: Comparison of the MLE and the partial envelope estimator for components of interest in Example 1

$g(\hat{\tau}_{\text{env}})$	$\hat{se}(g(\hat{\tau}_{\text{env}}))$	$g(\hat{\tau}_{\text{MLE}})$	$\hat{se}(g(\hat{\tau}_{\text{MLE}}))$	ratio
8.556	0.174	8.701	0.260	1.491
9.014	0.111	8.939	0.135	1.222
7.817	0.414	8.054	0.442	1.069
9.174	0.163	9.193	0.170	1.045
9.018	0.113	9.120	0.128	1.133
8.612	0.162	8.518	0.278	1.709
7.761	0.215	8.096	0.331	1.534

all of the ratios are greater than 1 which indicates that the envelope estimator of expected Darwinian fitness is less variable than the maximum likelihood estimator.

Contour plots of the ratios of estimated standard errors are displayed in the technical report. These contour plots show that the envelope estimator of expected Darwinian fitness is less variable than the maximum likelihood estimator for the majority of the observed data. The region where the envelope estimator is less variable includes the values of z_1 and z_2 that maximize estimated expected Darwinian fitness. Variance reduction is also obtained when we use the reducing subspace suggested by AIC. This is also shown in the accompanying technical report.

$$1 \rightarrow Y_1 \rightarrow Y_2$$

Figure 6: Graphical structure of the aster model for the data in Example 2. The first arrow corresponds to survival which is a Bernoulli random variable. The second arrow corresponds to reproduction count conditional on survival which is a zero-truncated Poisson random variable.

Table 2: Comparison of the MLE and the partial envelope estimator for components of interest in Example 2

$g(\hat{\tau}_{\text{env}})$	$\hat{se}(g(\hat{\tau}_{\text{env}}))$	$g(\hat{\tau}_{\text{MLE}})$	$\hat{se}(g(\hat{\tau}_{\text{MLE}}))$	ratio
9.646	0.326	9.171	0.642	1.973
8.640	0.300	8.887	0.369	1.230
7.659	0.315	7.603	0.361	1.144
7.517	0.539	7.010	0.649	1.205
10.943	0.607	10.475	0.896	1.476
7.329	0.707	6.618	1.038	1.469
7.498	0.521	7.522	0.658	1.263

5.2 Example 2

In this example we apply our envelope methods to a real aster dataset. The data comes from Lowry and Willis (2010) and the study in which the data is obtained investigates the role of chromosomal inversions in adaptation and speciation. Phenotypic traits and covariates are recorded for 2313 yellow monkeyflowers, *Mimulus guttatus*. The lifecycle of the individual *M. guttatus* flowers is depicted in Figure 6. The covariates of interest include genetic background, field site, inversion orientation, and ecotype of the flower. All of the considered covariates are categorical. We fit the main effects only model and find substantial gains with our methods. There are eight predictors in total and we partition τ into $(\gamma^T, v^T)^T$ where $\gamma \in \mathbb{R}^2$ are nuisance parameters and $v \in \mathbb{R}^6$ are relevant to the estimation of expected Darwinian fitness. AIC, BIC, and the LRT at $\alpha = 0.05$ all select a reducing subspace that is the sum of all eigenspaces of $\hat{\Sigma}_{v,v}$ with the exception of the fourth and fifth eigenspaces. The bootstrap procedure given in Figure 4 is used to estimate the variability of the envelope estimator of \hat{v} accounting for uncertainty in model selection. Table 2 shows points that yield high values of estimated expected Darwinian fitness. We can see that all of the ratios are greater than 1 which indicates that the envelope estimator of expected Darwinian fitness is less variable than the maximum likelihood estimator.

6 Envelope methods with respect to β

As already discussed, the aster model mean-value parameter τ is closely associated with mean-value parameter μ , see Figure 2 and consult Geyer, C. J. (2010) for more details about the six aster model parameterizations. One could also perform envelope methodology to estimate model canonical parameter vector β , which possesses the same dimension as τ . In our experience, envelope methodology with respect to β is computationally faster.

The computational benefit of using envelope methodology with respect to β is countered by an important drawback. Aster model theory is developed to handle the relation between β and relevant predictors in the form of an affine model. Therefore, the canonical parameter vector β is not well-defined, one can shift β with an arbitrarily chosen offset vector without changing the value of the mean-value parameters τ and μ . Envelope methodology is not invariant to this form of arbitrary shifting. It is true that `aster` and `aster2` software have a default way of picking offsets. However, the conventions of `aster` and `aster2` differ and experienced users of this software can also change offsets as they see fit. It should be noted that τ can also be shifted via an arbitrarily chosen offset vector. However, when one changes τ in this manner, one changes the definition of Darwinian fitness. Darwinian fitness, and surrogates to Darwinian fitness that are used in its place, are well-defined quantities.

7 Software

This paper is accompanied by an R package `envlpaster` and a technical report (see Supplementary Material Section). This technical report reproduces the examples in this paper and shows how functions in the `envlpaster` package are used.

8 Discussion

There are two types of errors that can be made when constructing envelope estimators and these two errors have very different consequences. The first error we could make is picking

an envelope dimension smaller than the truth. Conditional on this dimension, the resulting envelope estimator is no longer consistent, and the first defining condition of the envelope space is violated. Alternatively, an envelope dimension larger than the truth can be chosen. Conditional on this type of dimension, the envelope estimator is consistent but it will have higher variability than the envelope estimator constructed from the true envelope dimension. Efficiency gains are still possible in this setting as seen in the first example.

The consequences of potential model selection errors served as the motivation for the implementation of the bootstrap procedure in Efron (2014). However, this particular choice of a bootstrap procedure is not without flaws. Hjort (2014) mentions that Efron does not derive the distribution of the final estimator, given by (4) in our context. The literature has not reached a consensus on the appropriate bootstrap procedure to be implemented when bootstrapping depends on data-driven model selection. Berk, et al. (2013) provides an estimation framework that is valid under all model selection criteria, but the degree of conservatism guaranteed in Berk, et al. (2013) is not required in our setting. Other applications of envelope methodology may require this degree of conservatism. As the literature currently stands, Efron (2014) provides a reasonable solution to the problem of potential model selection errors in the application of envelope methodology to aster models. Our software also provides functions implementing bootstrap procedures not accounting for model selection.

The new envelope estimator constructed from reducing subspaces is seen to perform better than the envelope estimator constructed from the 1D algorithm in our first example. This new envelope estimator does not involve any non-convex optimization routines that are both sensitive to starting values and have potential problems with local minima. The underlying theory of the 1D algorithm justifies the consistency of our new envelope estimator. In envelope modeling problems with a small number of parameters of interest, possibly outside of our aster modeling context, the envelope estimator constructed from reducing subspaces has the potential to yield efficiency gains without the present worries of the current envelope estimation techniques.

In many life history analyses, specific trait values which are estimated to produce the

highest expected Darwinian fitness are of interest. It is common practice to only report such trait values (Shaw and Geyer, 2010; Eck et al., 2015). Such reporting ignores the variability associated with the estimation of expected Darwinian fitness. There are likely many trait values having estimated expected Darwinian fitness that is statistically indistinguishable from the reported values. Our methodology addresses this concern directly. The potential set of candidate traits maximizing expected Darwinian fitness is smaller when the combination of envelope methodology into the aster modeling framework is utilized as seen in the accompanying technical report.

The aster model has been solely applied to problems in life history analysis. However, the aster model is a general statistical model which can analyze datasets outside of the life history context. The aster model itself is a generalization of the generalized linear model (Shaw, Geyer, Wagenius, Hangelbroek, and Etterson, 2008) and survival models (Geyer, Wagenius, and Shaw, 2007). The aster model is appropriate for any graphical modeling problem meeting the assumptions A1-A5 or the more general assumptions of Geyer, et al. (2007).

Our main emphasis is to show that expected Darwinian fitness can be estimated with lower variability through the incorporation of general envelope methodology with respect to aster model parameters. A combination of the theories of aster and envelope models show that lower variability in estimation is obtainable. Our examples offer further support to our claims. The envelope estimator of expected Darwinian fitness is seen to be usefully less variable than the MLE. The variance reduction of estimated expected Darwinian fitness obtained through our methodology has the potential to be massive. Researchers using our methods will be able to draw strong inferences about expected Darwinian fitness through our variance reduction techniques.

Supplementary Materials

The accompanying technical report is available at the UMN Digital Conservancy (Eck, Geyer, and Cook, 2016). The calculations in the accompanying technical report are facilitated by the R pack-

age `envlpaster` (Eck, 2015).

Daniel J. Eck email: eckxx049@stat.umn.edu address: 313 Ford Hall, 224 Church St SE, Minneapolis, MN 55455

Charles J. Geyer email: charlie@stat.umn.edu

R. Dennis Cook email: dennis@stat.umn.edu

References

- Berk, R., Brown, L., Buja, A., Zhang, K., and Zhao, L. (2013). Valid post-selection inference. *Annals of Statistics*, **41**, 2, 802–837.
- Burger, R. and Lynch, M. (1995). Evolution and Extinction in a Changing Environment: A Quantitative-Genetic Analysis. *Evolution*, **49**, 151–163.
- Cook, R. D., Li, B., Chiaromonte, F. (2010). Envelope models for parsimonious and efficient multivariate linear regression. *Statistica Sinica*, **20**: 927-1010.
- Cook, R. D., Zhang, X. (2015). Algorithms for Envelope Estimation. *Journal of Computational and Graphical Statistics*, Published online. DOI:10.1080/10618600.2015.1029577.
- Cook, R. D., Zhang, X. (2015). Foundations for Envelope Models and Methods. *Journal of the American Statistical Association*, **110:510**: 599-611.
- Eck, D. J., Shaw, R., Geyer, C. J., Kingsolver J. G. (2015). An Integrated Analysis of Phenotypic Selection on Insect Body Size and Development Time. *Evolution*, **69**: 2525-2532.
- Eck, D. J., Geyer, C. J., and Cook, R. D. (2017). An Application of Envelope and Aster Models. *Submitted*.
- Eck, D. J. (2015). R package `envlpaster`, version 0.1-2. <http://cran.r-project.org/package=envlpaster>.

- Eck, D. J., Geyer, C. J., and Cook, R. D. (2016). Supporting Data Analysis for “An Application of Envelope Methodology and Aster Models.” <http://hdl.handle.net/11299/178384>.
- Efron, B. (2014). Estimation and Accuracy After Model Selection. *Journal of the American Statistical Association*, **109:507**: 991-1007.
- Etterson, J. R. and Shaw, R. G. (2001) Constraint to Adaptive Evolution in Response to Global Warming. *Science*, **294**, 151–154.
- Geyer, C. J., Wagenius, S., Shaw, R. G. (2007). Aster models for life history analysis. *Biometrika*, **94**: 415-426.
- Geyer, C. J. and Shaw, R. G. (2009). Model Selection in Estimation of Fitness Landscapes. Technical Report No. 671. School of Statistics, University of Minnesota. <http://conservancy.umn.edu/handle/11299/56219>.
- Geyer, C. J. (2010). A Philosophical Look at Aster Models. Technical Report No. 676. School of Statistics, University of Minnesota. <http://purl.umn.edu/57163>.
- Geyer, C. J. (2010). R package `aster2` (Aster Models), version 0.1. <http://cran.r-project.org/package=aster2>.
- Geyer, C. J. (2014). R package `aster` (Aster Models), version 0.8-30. <http://cran.r-project.org>.
- Hjort, N. L. (2014). Discussion of Efrons paper, Estimation and accuracy after model selection. *Journal of the American Statistical Association*, **109:507**, 1017–1020.
- Lande, R., Arnold, S. (1983). The measurement of selection on correlated characters. *Evolution*, **37**: 1210-1226.
- Lowry, D. B. and Willis, J. H. (2010). A Widespread Chromosomal Inversion Polymorphism Contributes to a Major Life-History Transition, Local Adaptation, and Reproductive. *PLoS Biol*, **8(9)**, e1000500, 10.1371/journal.pbio.1000500.

- Mitchell-Olds, T. and Shaw, R. G. (1987). Regression analysis of natural selection: statistical inference and biological interpretation. *Evolution*, **41**, 1149–1161.
- Shaw, R. G., Geyer, C. J., Wagenius, S., Hangelbroek, H., and Etterson, J. R. (2008). Unifying life-history analyses for inference of fitness and population growth. *The American Naturalist*, **172**: E35–E47.
- Shaw, R. G., Geyer, C. J. (2010). Inferring fitness landscapes. *Evolution*, **64**: 2510–2520.
- Su, Z. and Cook, R. D. (2011). Partial envelopes for efficient estimation in multivariate linear regression. *Biometrika*, **98**, 133–146.